

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: WASTFALT, Maria K. Boden
FLOCK, Jan-Ingmar
- (ii) TITLE OF INVENTION: FIBRINOGEN BINDING PROTEIN
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 - (B) STREET: P.O. Box 1404
 - (C) CITY: Alexandria
 - (D) STATE: Virginia
 - (E) COUNTRY: United States
 - (F) ZIP: 22313-1404
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: TBA (Div of US 09/276,141)
 - (B) FILING DATE: Even date herewith
 - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/276,141
 - (B) FILING DATE: 25-03-99
 - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/244,229
 - (B) FILING DATE: 09-DEC-1994
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: SE 9202720-0
 - (B) FILING DATE: 21-SEP-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: SE 9302955-1
 - (B) FILING DATE: 13-SEP-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: WO PCT/SE93/00759
 - (B) FILING DATE: 20-SEP-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: McGowan, Malcolm K.

TD/280-761835660

(B) REGISTRATION NUMBER: 39,300
(C) REFERENCE/DOCKET NUMBER: 012889-011

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (703) 836-6620
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ile Val Thr Lys Asp Tyr Ser Lys Glu Ser Arg Val Asn Glu Asn Ser
1 5 10 15
Lys Tyr Gly Thr
20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ile Val Thr Lys Asp Tyr Ser Lys Glu Ser Arg Val Asn Glu Lys Ser
1 5 10 15
Lys Lys Gly Ala
20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SEQ ID NO: 265354380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ile Val Thr Lys Asp Tyr Ser Gly Lys Ser Gln Val Asn Ala Gly Ser
1 5 10 15
Lys Asn Gly Thr
20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ile Val Thr Lys Asp Tyr Ser Gly Lys Ser Gln Val Asn Ala Gly Ser
1 5 10 15
Lys Asn Gly Thr
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His
1 5 10 15
Asn Ile Val Glu
20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Tyr Pro Glu Lys Lys Pro Val
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGCGAAGGA TACGGTCAA GAGAAAAGAA ACCAGTGAGT ATTAATCACA ATATCGTAGA	60
GTACAATGAT GGTACTTTA AATATCAATC TAGACCAAAA TTTAACTCAA CACCTAAATA	120
TATTAATTC AAACATGACT ATAATATTTT AGAATTTAAC GATGGTACAT TCGAATATGG	180
TGACACGTCCA CAATTTAATA AACCAGCAGC GAAAAGTGAT GCAACTATTA AAAAGAACAA	240
AAAATTGATT CAAGCTCAAA ATCTTGAG AGAATTTGAA AAAACACATA CTGTCAGTGC	300
ACACAGAAAA GCACAAAAGG CAGTCAACTT AGTTTCGTTT GAATACAAAG TGAAGAAAAT	360
GGTCTTACAA GAGCGAATTG ATAATGTATT AAAACAAGGA TTAGTGAG	408

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His	
1 5 10 15	
Asn Ile Val Glu Tyr Asn Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro	
20 25 30	
Lys Phe Asn Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn	
35 40 45	

Ile Leu Glu Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln
50 55 60

Phe Asn Lys Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln
65 70 75 80

Lys Leu Ile Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His
85 90 95

Thr Val Ser Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser
100 105 110

Phe Glu Tyr Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn
115 120 125

Val Leu Lys Gln Gly Leu Val Arg
130 135

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1009 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 157..654

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 804..1007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACTAGTGTAA TAAAGTGCCTGA TGAGTCACAA GATAGATAAC TATATTTGT CTATATTATA 60

AAAGTGTATTAT AGTTAATTAA TAATTTAGTTA ATTTCAAAAG TTGTATAAAAT AGGATAACTT 120

AATAAAATGTAA AGATAATAAT TTGGAGGATA ATTAAC ATG AAA AAT AAA TTG ATA 174

Met Lys Asn Lys Leu Ile
1 5

GCA AAA TCT TTA TTA ACA ATA GCG GCA ATT GGT ATT ACT ACA ACT ACA 222

Ala Lys Ser Leu Leu Thr Ile Ala Ala Ile Gly Ile Thr Thr Thr Thr
10 15 20

ATT GCG TCA ACA GCA GAT GCG AGC GAA GGA TAC GGT CCA AGA GAA AAG 270

Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro Arg Glu Lys
25 30 35

AAA CCA GTG AGT ATT AAT CAC AAT ATC GTA GAG TAC AAT GAT GGT ACT Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn Asp Gly Thr	318
40 45 50	
TTT AAA TAT CAA TCT AGA CCA AAA TTT AAC TCA ACA CCT AAA TAT ATT Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro Lys Tyr Ile	366
55 60 65 70	
AAA TTC AAA CAT GAC TAT AAT ATT TTA GAA TTT AAC GAT GGT ACA TTC Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp Gly Thr Phe	414
75 80 85	
GAA TAT GGT GCA CGT CCA CAA TTT AAT AAA CCA GCA GCG AAA ACT GAT Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala Lys Thr Asp	462
90 95 100	
GCA ACT ATT AAA AAA GAA CAA AAA TTG ATT CAA GCT CAA AAT CTT GTG Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln Asn Leu Val	510
105 110 115	
AGA GAA TTT GAA AAA ACA CAT ACT GTC AGT GCA CAC AGA AAA GCA CAA Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg Lys Ala Gln	558
120 125 130	
AAG GCA GTC AAC TTA GTT TCG TTT GAA TAC AAA GTG AAG AAA ATG GTC Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys Lys Met Val	606
135 140 145 150	
TTA CAA GAG CGA ATT GAT AAT GTA TTA AAA CAA GGA TTA GTG AGA TAA Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu Val Arg *	654
155 160 165	
TACTTCTGTC ATTATTTAA GTTCAAAATA ATTTAATATT ATATTATTT TTATTAATAA	714
AACGACTATG CTATTAATG CCAGGTTAAC GTAACTTCC TAAATTGAC TATATAATCG	774
TTAAGTATCA ATTTTAAGGA GAGTTTACA ATG AAA TTT AAA AAA TAT ATA TTA Met Lys Phe Lys Lys Tyr Ile Leu	827
1 5	
ACA GGA ACA TTA GCA TTA CTT TTA TCA TCA ACT GGG ATA GCA ACT ATA Thr Gly Thr Leu Ala Leu Leu Ser Ser Thr Gly Ile Ala Thr Ile	875
10 15 20	
GAA GGG AAT AAA GCA GAT GCA AGT AGT CTG GAC AAA TAT TTA ACT GAA Glu Gly Asn Lys Ala Asp Ala Ser Ser Leu Asp Lys Tyr Leu Thr Glu	923
25 30 35 40	
AGT CAG TTT CAT GAT AAA CGC ATA GCA GAA GAA TTA AGA ACT TTA CTT Ser Gln Phe His Asp Lys Arg Ile Ala Glu Glu Leu Arg Thr Leu Leu	971
45 50 55	

AAC AAA TCG AAT GTA TAT GCA TTA GCT GCA GGA AGC TT
Asn Lys Ser Asn Val Tyr Ala Leu Ala Ala Gly Ser
60 65

1009

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 781 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATAGATAACT ATATTTGTC TATATTATAA AGTGTGTTATA GTTAATTAAT AATTAGTTAA 60
TTTCAAAAGT TGTATAAATAA GGATAACTTA ATAAATGTAA GATAATAATT TGGAGGATAA 120
TTAACATGAA AAATAAATTG ATAGCAAAT CTTTATTAAC AATAGCGGCA ATTGGTATTA 180
CTACAACTAC AATTGCGTCA ACAGCAGATG CGAGCCAAGG ATACGGTCCA AGAGAAAAGA 240
AACCACTGAG TATTAATCAC AATATCGTAG AGTACAATGA TGGTACTTTT AAATATCAAT 300
CTAGACAAA ATTTAACTCA ACACCTAAAT ATATTAATT CAAACATGAC TATAATATT 360
TAGAATTAA CGATGGTACA TTCGAATATG GTGCACGTCC ACAATTAAAT AAACAGCAG 420
CGAAAACTGA TGCAACTTATT AAAAAAGAAC AAAAATTGAT TCAAGCTCAA AATCTTGTGA 480
GAGAATTGAA AAAAACACAT ACTGTCAGTG CACACAGAAA AGCACAAAAG GCAGTCAACT 540
TAGTTTCGTT TGAATACAAA GTCAAGAAAA TGGTCTTACA AGAGCGAATT GATAATGTAT 600
TAAACAAAGG ATTAGTGAGA TAATACTTCT GTCATTATTT TAAGTTCAA ATAATTAAAT 660
ATTATATTAT TTTTATTA AAAAAAGACT ATGCTATTAA ATGCCAGGTT AATGTAACCT 720
TCCTAAAATT GACTATATAA TCGTTAAGTA TCAATTAAAGGAGAGTTA CAATGAAATT 780
T 781

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 785 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATAGATAGCT ATATTCAGTC TATATTATAA AGTGTGTTATA GTTAATTAAAT AATTAGTTAA	60
TTTCAAAAGT TGTATAAATAA GGATAACTTA ATAATGTAA GATAATAATT TGGAGGATAA	120
TTGACATGAA AAATGCATTG ATAGCAAAAT CTTTATTAAAC ATTAGCGGCA ATAGGTATTA	180
CTACAACTAC AATTGCGTCA ACAGCAGATG CGAGCGAAGG ATACGGTCCA AGAGAAAAGA	240
AACCACTGAG TATTAATCAC AATATCGTAG AGTACAATGA TGGTACTTTT AAATATCAAT	300
CTAGACCAAA ATTTAACTCA ACACCTAAAT ATATTAAATT CAAACATGAC TATAATATTT	360
TAGAATTAA CGATGGTACA TTGCAATATG GTGCACGTCC ACAATTAAAT AAACCAAGCAG	420
CGAAAACATGA TGCAACTATT AAAAAGAAC AAAAATTGAT TCAAGCTCAA AATTTGTGA	480
GAGAATTGAA AAAAACACAT ACTGTCAGTG CACACAGAAA AGCACAAAAG GCAGTCAACT	540
TAGTTTCGTT TGAATACAAA GTGAAGAAAA TGGTCTTACA AGAGCGAATT GATAATGTAT	600
TAAAACAAAGG ATTAGTTAAA TAAAACATTCA ATCGTTGCTG TTATCTGGAA ATAATTAATT	660
AAATGTTATG TTAATTTTG TTAATGAAAA AAGTAATCTA TTTAATGACA GGTAAATGTA	720
ATTGTCCTGA AATTGACTAT ATATCAGTA AGTATCAATT TTAAGGAGAG CTTATAATGTA	780
AATT	785

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Lys Asn Lys Leu Ile Ala Lys Ser Leu Leu Thr Ile Ala Ala Ile			
1	5	10	15

Gly Ile Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly		
20	25	30

Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val		
35	40	45

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Lys Asn Ala Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile
1 5 10 15

Gly Ile Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly
20 25 30

Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val
 35 40 45

Glu Tyr Asn Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn
 50 55 60

Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu
 65 70 75 80

Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys
85 90 95

Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile
100 105 110

Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser
115 120 125

Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr
130 135 140

Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys
145 150 155 160

Gln Gly Leu Val Lys
165

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His
1 5 10 15

Asn Ile Val Glu Tyr Asn Asp Gly Ser Phe Lys Tyr Gln Ser Arg Pro
20 25 30

Lys Phe Asn Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn
35 40 45

Ile Leu Glu Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln
50 55 60

Phe Asn Lys Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln
65 70 75 80

Lys Leu Ile Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His
85 90 95

Thr Val Ser Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser
100 105 110

Phe Glu Tyr Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn
115 120 125

Val Leu Lys Gln Gly Leu Val Arg
130 135

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Ser Gln Tyr Gly Pro Arg Pro Gln Phe Asn Lys Thr Pro Lys Tyr
1 5 10 15

Val Lys Tyr Arg Asp Ala Gly Thr Gly Ile Arg Glu Tyr Asn Asp Gly
20 25 30

Thr Phe Gly Tyr Glu Ala Arg Pro Arg Phe Asn Lys Pro Ser Glu Thr
35 40 45

Asn Ala Tyr Asn Val Thr Thr His Ala Asn Gly Gln Val Ser Tyr Gly
50 55 60

Ala Arg Pro Thr Tyr Lys Lys Pro Ser Glu Thr Asn Ala Tyr Asn Val
65 70 75 80

Thr Thr His Ala Asn Gly Gln Val Ser Tyr Gly Ala Arg Pro Thr Gln
85 90 95

Asn Lys Pro Ser Glu Thr Asn Ala Tyr Asn Val Thr Thr His Gly Asn
100 105 110

Gly Gln Val Ser Tyr Gly Ala Arg Gln Ala Gln Asn Lys Pro Ser Lys
115 120 125

Thr Asn Ala Tyr Asn Val Thr Thr His Ala Asn Gly Gln Val Ser Tyr
130 135 140

Gly Ala Arg Pro Thr Tyr Lys Lys Pro Ser Lys Thr Asn Ala Tyr Asn
145 150 155 160

Val Thr Thr His Ala Asp Gly Thr Ala Thr Tyr Gly Pro Arg Val Thr
165 170 175

Lys

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